



Query= SEQ ID NO:1  
(426 letters)

Sequences producing significant alignments:

AC024580.6.1.193609

Score (bits)	E Value
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299 7e-79

>AC024580.6.1.193609  
Length = 193609

Score = 299 bits (151), Expect = 7e-79  
Identities = 151/151 (100%)  
Strand = Plus / Plus

Query: 220 gggctccctactcccaccctccacagccctccaagaggaatgtgatggagacgttgcc 279  
Sbjct: 178486 gggctccctactcccaccctccacagccctccaagaggaatgtgatggagacgttgcc 178545

Query: 280 aaaccagagattggaggtaaaggccaggaaacacagaagagagacaccgacaggaggggg 339  
Sbjct: 178546 aaaccagagattggaggtaaaggccaggaaacacagaagagagacaccgacaggaggggg 178605

Query: 340 gaacaaggaagtggcaggcagagcttagagg 370  
Sbjct: 178606 gaacaaggaagtggcaggcagagcttagagg 178636

Score = 174 bits (88), Expect = 3e-41  
Identities = 88/88 (100%)  
Strand = Plus / Plus

Query: 1 atggctcctccctccgtccccctggtcctccctcgctcttgcgtgacgcctggcagag 60  
Sbjct: 172458 atggctcctccctccgtccccctggtcctccctcgctcttgcgtgacgcctggcagag 172517

Query: 61 actccagcatccgcacctgcccacccggg 88  
Sbjct: 172518 actccagcatccgcacctgcccacccggg 172545

Score = 163 bits (82), Expect = 1e-37  
Identities = 82/82 (100%)  
Strand = Plus / Plus

Query: 136 gtctccaccccccataatgggtgaccaagacggaaagagggagacagcccttgagatc 195  
Sbjct: 177520 gtctccaccccccataatgggtgaccaagacggaaagagggagacagcccttgagatc 177579

Query: 196 ctagacctgtggaaggccatcg 217  
|||||||  
Sbjct: 177580 ctagacctgtggaaggccatcg 177601

Score = 113 bits (57), Expect = 9e-23  
Identities = 57/57 (100%)  
Strand = Plus / Plus

Query: 370 gatctggcatgctcagcatgaaaattcccaaggaggaagatgtcctgaagtcatag 426  
|||||||  
Sbjct: 180563 gatctggcatgctcagcatgaaaattcccaaggaggaagatgtcctgaagtcatag 180619

Score = 99.6 bits (50), Expect = 1e-18  
Identities = 50/50 (100%)  
Strand = Plus / Plus

Query: 87 gggacgaggaggctggaccctcaatagtgctggcaccttctgggtcccg 136  
|||||||  
Sbjct: 175934 gggacgaggaggctggaccctcaatagtgctggcaccttctgggtcccg 175983